

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: RAMESCH V. NAIR
MARK S. PAYNE
DONALD E. TRIMBUR
FERNANDO VALLE
- (ii) TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
GLYCEROL BY RECOMBINANT
ORGANISMS
- (iii) NUMBER OF SEQUENCES: 43
- (iv) CORRESPONDENCE ADDRESS:
(A) NAME: E. I. DU PONT DE NEMOURS AND COMPANY
(B) STREET: 1007 MARKET STREET
(C) CITY: WILMINGTON
(D) STATE: DELAWARE
(E) COUNTRY: U.S.A.
(F) ZIP: 19898

(A) ADDRESSEE: GENENCOR INTERNATIONAL, INC.
(B) STREET: 4 CAMBRIDGE PLACE
1870 SOUTH WINTON ROAD
(C) CITY: ROCHESTER
(D) STATE: NEW YORK
(E) COUNTRY: U.S.A.
(F) ZIP: 14618
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: DISKETTE, 3.5 INCH
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: MICROSOFT WINDOWS 95
(D) SOFTWARE: MICROSOFT WORD VERSION 7.0A
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/030602
(B) FILING DATE: NOVEMBER 13, 1996
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: FLOYD, LINDA AXAMETHY
(B) REGISTRATION NUMBER: 33,692
(C) REFERENCE/DOCKET NUMBER: CR-9981-B
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 302-892-8112
(B) TELEFAX: 302-773-0164

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTTTAATTTT CTTTTATCTT ACTCTCCTAC ATAAGACATC AAGAAACAAT TGTATATTGT 60
ACACCCCCC CCTCCACAAA CACAAATATT GATAATATAA AGATGTCTGC TGCTGCTGAT 120
AGATTAAACT TAACTTCCGG CCACTTGAAT GCTGGTAGAA AGAGAAGTTC CTCTTCTGTT 180
TCTTTGAAGG CTGCCGAAAA GCCTTTCAAG GTTACTGTGA TTGGATCTGG TAACTGGGGT 240
ACTACTATTG CCAAGGTGGT TGCCGAAAAT TGTAAGGGAT ACCCAGAAGT TTTCGCTCCA 300
ATAGTACAAA TGTGGGTGTT CGAAGAAGAG ATCAATGGTG AAAAATTGAC TGAAATCATA 360
AATACTAGAC ATCAAAACGT GAAATACTTG CCTGGCATCA CTCTACCCGA CAATTTGGTT 420
GCTAATCCAG ACTTGATTGA TTCAGTCAAG GATGTCGACA TCATCGTTTT CAACATTCCA 480
CATCAATTTT TGCCCCGTAT CTGTAGCCAA TTGAAAGGTC ATGTTGATTC ACACGTCAGA 540
GCTATCTCCT GTCTAAAGGG TTTTGAAGTT GGTGCTAAAG GTGTCCAATT GCTATCCTCT 600
TACATCACTG AGGAACTAGG TATTCAATGT GGTGCTCTAT CTGGTGCTAA CATTGCCACC 660
GAAGTCGCTC AAGAACTAGT GTCTGAAACA ACAGTTGCTT ACCACATTCC AAAGGATTTT 720
AGAGGCGAGG GCAAGGACGT CGACCATAAG GTTCTAAAGG CCTTGTTCCA CAGACCTTAC 780
TTCCACGTTA GTGTCATCGA AGATGTTGCT GGTATCTCCA TCTGTGGTGC TTTGAAGAAC 840
GTTGTTGCCT TAGGTTGTGG TTTCGTCGAA GGTCTAGGCT GGGGTAACAA CGCTTCTGCT 900
GCCATCCAAA GAGTCGGTTT GGGTGAGATC ATCAGATTCG GTCAAATGTT TTTCCAGAA 960
TCTAGAGAAG AACATACTA CCAAGAGTCT GCTGGTGTTG CTGATTTGAT CACCACCTGC 1020
GCTGGTGGTA GAAACGTCAA GGTTGCTAGG CTAATGGCTA CTTCTGGTAA GGACGCCTGG 1080
GAATGTGAAA AGGAGTTGTT GAATGGCCAA TCCGCTCAAG GTTTAATTAC CTGCAAAGAA 1140
GTTACGAAT GGTTGGAAAC ATGTGGCTCT GTCGAAGACT TCCCATTATT TGAAGCCGTA 1200
TACCAAATCG TTTACAACAA CTACCCAATG AAGAACCTGC CGGACATGAT TGAAGAATTA 1260
GATCTACATG AAGATTAGAT TTATTGGAGA AAGATAACAT ATCATACTTC CCCCACTTTT 1320
TTCGAGGCTC TTCTATATCA TATTCATAAA TTAGCATTAT GTCATTTCTC ATAECTACTT 1380

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2946 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCGAGC CTGAAGTGCT GATTACCTTC AGGTAGACTT CATCTTGACC CATCAACCCC 60
AGCGTCAATC CTGCAAATAC ACCACCCAGC AGCACTAGGA TGATAGAGAT AATATAGTAC 120
GTGGTAACGC TTGCCTCATC ACCTACGCTA TGGCCGGAAT CGGCAACATC CCTAGAATTG 180
AGTACGTGTG ATCCGGATAA CAACGGCAGT GAATATATCT TCGGTATCGT AAAGATGTGA 240
TATAAGATGA TGTATACCCA ATGAGGAGCG CCTGATCGTG ACCTAGACCT TAGTGGCAAA 300
AACGACATAT CTATTATAGT GGGGAGAGTT TCGTGCAAAT AACAGACGCA GCAGCAAGTA 360
ACTGTGACGA TATCAACTCT TTTTTTATTA TGTAATAAGC AAACAAGCAC GAATGGGGAA 420
AGCCTATGTG CAATCACCAA GGTCGTCCTT TTTTCCCAT TTGCTAATTT AGAATTTAAA 480
GAAACCAAAA GAATGAAGAA AGAAAACAAA TACTAGCCCT AACCCCTGACT TCGTTTCTAT 540
GATAATACCC TGCTTTAATG AACGGTATGC CCTAGGGTAT ATCTCACTCT GTACGTTACA 600
AACTCCGGTT ATTTTATCGG AACATCCGAG CACCCGCGCC TTCCTCAACC CAGGCACCGC 660
CCCAGGTAAC CGTGCGCGAT GAGCTAATCC TGAGCCATCA CCCACCCAC CCGTTGATGA 720
CAGCAATTCTG GGAGGGCGAA AATAAACTG GAGCAAGGAA TTACCATCAC CGTCACCATC 780
ACCATCATAT CGCCTTAGCC TCTAGCCATA GCCATCATGC AAGCGTGTAT CTTCTAAGAT 840
TCAGTCATCA TCATTACCGA GTTTGTTTTT CTTACATGA TGAAGAAGGT TTGAGTATGC 900
TCGAAACAAT AAGACGACGA TGGCTCTGCC ATTGGTTATA TTACGCTTTT GCGGCGAGGT 960
GCCGATGGGT TGCTGAGGGG AAGAGTGTTT AGCTTACGGA CCTATTGCCA TTGTTATTCC 1020
GATTAATCTA TTGTTGAGCA GCTCTTCTCT ACCCTGTCAT TCTAGTATTT TTTTTTTTTT 1080
TTTTTGTTTT TACTTTTTTT TCTTCTTGCC TTTTTTCTT GTTACTTTTT TTCTAGTTTT 1140
TTTTCCTTCC ACTAAGCTTT TTCCTTGATT TATCCTTGGG TTCTTCTTTC TACTCCTTTA 1200
GATTTTTTTT TTATATATTA ATTTTAAAGT TTATGTATTT TGGTAGATTC AATTCTCTTT 1260
CCCTTTCCTT TTCCTTCGCT CCCCTTCCTT ATCAATGCTT GCTGTCAGAA GATTAACAAG 1320
ATACACATTC CTTAAGCGAA CGCATCCGGT GTTATATACT CGTCGTGCAT ATAAAATTTT 1380

GCCTTCAAGA	TCTACTTTCC	TAAGAAGATC	ATTATTACAA	ACACAACGTC	ACTCAAAGAT	1440
GACTGCTCAT	ACTAATATCA	AACAGCACAA	ACACTGTCAT	GAGGACCATC	CTATCAGAAG	1500
ATCGGACTCT	GCCGTGTCAA	TTGTACATTT	GAAACGTGCG	CCCTTCAAGG	TTACAGTGAT	1560
TGGTTCTGGT	AACTGGGGGA	CCACCATCGC	CAAAGTCATT	GCGGAAAACA	CAGAATTGCA	1620
TTCCCATATC	TTCGAGCCAG	AGGTGAGAAT	GTGGGTTTTT	GATGAAAAGA	TCGGCGACGA	1680
AAATCTGACG	GATATCATAA	ATACAAGACA	CCAGAACGTT	AAATATCTAC	CCAATATTGA	1740
CCTGCCCCAT	AATCTAGTGG	CCGATCCTGA	TCTTTTACAC	TCCATCAAGG	GTGCTGACAT	1800
CCTTGTTTTT	AACATCCCTC	ATCAATTTTT	ACCAAACATA	GTCAAACAAT	TGCAAGGCCA	1860
CGTGGCCCCT	CATGTAAGGG	CCATCTCGTG	TCTAAAAGGG	TTCGAGTTGG	GCTCCAAGGG	1920
TGTGCAATTG	CTATCCTCCT	ATGTTACTGA	TGAGTTAGGA	ATCCAATGTG	GCGCACTATC	1980
TGGTGCAAAC	TTGGCACC GG	AAGTGGCCAA	GGAGCATTGG	TCCGAAACCA	CCGTGGCTTA	2040
CCAACTACCA	AAGGATTATC	AAGGTGATGG	CAAGGATGTA	GATCATAAGA	TTTTGAAATT	2100
GCTGTTCCAC	AGACCTTACT	TCCACGTCAA	TGTCATCGAT	GATGTTGCTG	GTATATCCAT	2160
TGCCGGTGCC	TTGAAGAACG	TCGTGGCACT	TGCATGTGGT	TTCGTAGAAG	GTATGGGATG	2220
GGGTAACAAT	GCCTCCGCAG	CCATTCAAAG	GCTGGGTTTA	GGTGAAATTA	TCAAGTTCGG	2280
TAGAATGTTT	TTCCCAGAAT	CCAAAGTCGA	GACCTACTAT	CAAGAATCCG	CTGGTGTTGC	2340
AGATCTGATC	ACCACCTGCT	CAGGCGGTAG	AAACGTCAAG	GTTGCCACAT	ACATGGCCAA	2400
GACCGGTAAG	TCAGCCTTGG	AAGCAGAAAA	GGAATTGCTT	AACGGTCAAT	CCGCCCAAGG	2460
GATAATCACA	TGCAGAGAAG	TTCACGAGTG	GCTACAAACA	TGTGAGTTGA	CCCAAGAATT	2520
CCCAATTATT	CGAGGCAGTC	TACCAGATAG	TCTACAACAA	CGTCCGCATG	GAAGACCTAC	2580
CGGAGATGAT	TGAAGAGCTA	GACATCGATG	ACGAATAGAC	ACTCTCCCCC	CCCCCTCCCC	2640
TCTGATCTTT	CCTGTTGCCT	CTTTTTCCCC	CAACCAATTT	ATCATTATAC	ACAAGTTCTA	2700
CAACTACTAC	TAGTAACATT	ACTACAGTTA	TTATAATTTT	CTATTCTCTT	TTTCTTTAAG	2760
AATCTATCAT	TAACGTTAAT	TTCTATATAT	ACATAACTAC	CATTATACAC	GCTATTATCG	2820
TTTACATATC	ACATCACCGT	TAATGAAAGA	TACGACACCC	TGTACACTAA	CACAAATAAA	2880
TAATCGCCAT	AACCTTTTCT	GTTATCTATA	GCCCTTAAAG	CTGTTTCTTC	GAGCTTTTCA	2940
CTGCAG						2946

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3178 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGCAGAACT	TCGTCTGCTC	TGTGCCCATC	CTCGCGGTTA	GAAAGAAGCT	GAATTGTTTC	60
ATGCGCAAGG	GCATCAGCGA	GTGACCAATA	ATCACTGCAC	TAATTCCTTT	TTAGCAACAC	120
ATACTTATAT	ACAGCACCAG	ACCTTATGTC	TTTTCTCTGC	TCCGATACGT	TATCCCACCC	180
AACTTTTATT	TCAGTTTTGG	CAGGGGAAAT	TTCACAACCC	CGCACGCTAA	AAATCGTATT	240
TAAACTTAAA	AGAGAACAGC	CACAAATAGG	GAACCTTGGT	CTAAACGAAG	GACTCTCCCT	300
CCCTTATCTT	GACCGTGCTA	TTGCCATCAC	TGCTACAAGA	CTAAATACGT	ACTAATATAT	360
GTTTTTCGGTA	ACGAGAAGAA	GAGCTGCCGG	TGCAGCTGCT	GCCATGGCCA	CAGCCACGGG	420
GACGCTGTAC	TGGATGACTA	GCCAAGGTGA	TAGGCCGTTA	GTGCACAATG	ACCCGAGCTA	480
CATGGTGCAA	TTCCCCACCG	CCGCTCCACC	GGCAGGTCTC	TAGACGAGAC	CTGCTGGACC	540
GTCTGGACAA	GACGCATCAA	TTCGACGTGT	TGATCATCGG	TGGCGGGGCC	ACGGGGACAG	600
GATGTGCCCT	AGATGCTGCG	ACCAGGGGAC	TCAATGTGGC	CCTTGTTGAA	AAGGGGGATT	660
TTGCCTCGGG	AACGTCGTCC	AAATCTACCA	AGATGATTCA	CGGTGGGGTG	CGGTACTTAG	720
AGAAGGCCTT	CTGGGAGTTC	TCCAAGGCAC	AACTGGATCT	GGTCATCGAG	GCACTCAACG	780
AGCGTAAACA	TCTTATCAAC	ACTGCCCTC	ACCTGTGCAC	GGTGCTACCA	ATTCTGATCC	840
CCATCTACAG	CACCTGGCAG	GTCCCGTACA	TCTATATGGG	CTGTAAATTC	TACGATTTCT	900
TTGGCGGTTT	CCAAAATTG	AAAAAATCAT	ACCTACTGTC	CAAATCCGCC	ACCGTGGAGA	960
AGGCTCCCAT	GCTTACCACA	GACAATTTAA	AGGCCTCGCT	TGTGTACCAT	GATGGGTCCT	1020
TTAACGACTC	GCGTTTGAAC	GCCACTTTAG	CCATCACGGG	TGTGGAGAAC	GGCGCTACCG	1080
TCTTGATCTA	TGTCGAGGTA	CAAAAATTGA	TCAAAGACCC	AACTTCTGGT	AAGGTTATCG	1140
GTGCCGAGGC	CCGGGACGTT	GAGACTAATG	AGCTTGTCAG	AATCAACGCT	AAATGTGTGG	1200
TCAATGCCAC	GGGCCCATAC	AGTGACGCCA	TTTTGCAAAT	GGACCGCAAC	CCATCCGGTC	1260
TGCCGGACTC	CCCGCTAAAC	GACAACTCCA	AGATCAAGTC	GACTTTCAAT	CAAATCTCCG	1320
TCATGGACCC	GAAAATGGTC	ATCCCATCTA	TTGGCGTTCA	CATCGTATTG	CCCTCTTTTT	1380
ACTCCCCGAA	GGATATGGGT	TTGTTGGACG	TCAGAACCTC	TGATGGCAGA	GTGATGTTCT	1440
TTTACCTTG	GCAGGGCAAA	GTCCTTGCCG	GCACCACAGA	CATCCCCTA	AAGCAAGTCC	1500

CAGAAAACCC TATGCCTACA GAGGCTGATA TTCAAGATAT CTTGAAAGAA CTACAGCACT 1560
 ATATCGAATT CCCCGTGAAA AGAGAAGACG TGCTAAGTGC ATGGGCTGGT GTCAGACCTT 1620
 TGGTCAGAGA TCCACGTACA ATCCCCGCAG ACGGGAAGAA GGGCTCTGCC ACTCAGGGCG 1680
 TGGTAAGATC CCACTTCTTG TTTCACTTCGG ATAATGGCCT AATTACTATT GCAGGTGGTA 1740
 AATGGACTAC TTACAGACAA ATGGCTGAGG AAACAGTCGA CAAAGTTGTC GAAGTTGGCG 1800
 GATTCCACAA CCTGAAACCT TGTCACACAA GAGATATTAA GCTTGCTGGT GCAGAAGAAT 1860
 GGACGCAAAA CTATGTGGCT TTATTGGCTC AAAACTACCA TTTATCATCA AAAATGTCCA 1920
 ACTACTTGGT TCAAACTAC GGAACCCGTT CCTCTATCAT TTGCGAATTT TTCAAAGAAT 1980
 CCATGGAAAA TAAACTGCCT TTGTCCTTAG CCGACAAGGA AAATAACGTA ATCTACTCTA 2040
 GCGAGGAGAA CAACTTGGTC AATTTTGATA CTTTCAGATA TCCATTCACA ATCGGTGAGT 2100
 TAAAGTATTC CATGCAGTAC GAATATTGTA GAACTCCCTT GGAATTCCTT TTAAGAAGAA 2160
 CAAGATTCGC CTTCTTGGAC GCCAAGGAAG CTTTGAATGC CGTGCATGCC ACCGTCAAAG 2220
 TTATGGGTGA TGAGTTCAAT TGGTCGGAGA AAAAGAGGCA GTGGGAACTT GAAAAAACTG 2280
 TGAACATTCAT CCAAGGACGT TTCGGTGTCT AAATCGATCA TGATAGTTAA GGGTGACAAA 2340
 GATAACATTC ACAAGAGTAA TAATAATGGT AATGATGATA ATAATAATAA TGATAGTAAT 2400
 AACAATAATA ATAATGGTGG TAATGGCAAT GAAATCGCTA TTATTACCTA TTTTCCTTAA 2460
 TGGAAGAGTT AAAGTAAACT AAAAAAACTA CAAAAATATA TGAAGAAAAA AAAAAAAGA 2520
 GGTAATAGAC TCTACTACTA CAATTGATCT TCAAATTATG ACCTTCCTAG TGTTTATATT 2580
 CTATTTCCAA TACATAATAT AATCTATATA ATCATTGCTG GTAGACTTCC GTTTTAATAT 2640
 CGTTTTAATT ATCCCCTTTA TCTCTAGTCT AGTTTTATCA TAAAATATAG AAACACTAAA 2700
 TAATATTCTT CAAACGGTCC TGGTGCATAC GCAATACATA TTTATGGTGC AAAAAAAAAA 2760
 ATGGAAAATT TTGCTAGTCA TAAACCCTTT CATAAAACAA TACGTAGACA TCGCTACTTG 2820
 AAATTTTCAA GTTTTTATCA GATCCATGTT TCCTATCTGC CTTGACAACC TCATCGTCGA 2880
 AATAGTACCA TTTAGAACGC CCAATATTCA CATTGTGTTT AAGGTCTTTA TTCACCAGTG 2940
 ACGTGTAATG GCCATGATTA ATGTGCCTGT ATGGTTAACC ACTCCAAATA GCTTATATTT 3000
 CATAGTGTC AATTGTTTTCA ATATAATGTT TAGTATCAAT GGATATGTTA CGACGGTGTT 3060
 ATTTTCTTG GTCAAATCGT AATAAAATCT CGATAAATGG ATGACTAAGA TTTTGGTAA 3120
 AGTTACAAAA TTTATCGTTT TCACTGTTGT CAATTTTTTG TTCTTGTAAT CACTCGAG 3178

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 816 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGAAACGTT TCAATGTTTT AAAATATATC AGAACAACAA AAGCAAATAT ACAAACCATC 60
GCAATGCCTT TGACCACAAA ACCTTTATCT TTGAAAATCA ACGCCGCTCT ATTCGATGTT 120
GACGGTACCA TCATCATCTC TCAACCAGCC ATTGCTGCTT TCTGGAGAGA TTTCGGTAAA 180
GACAAGCCTT ACTTCGATGC CGAACACGTT ATTCACATCT CTCACGGTTG GAGAACTTAC 240
GATGCCATTG CCAAGTTCGC TCCAGACTTT GCTGATGAAG AATACGTAA CAAGCTAGAA 300
GGTGAAATCC CAGAAAAGTA CGGTGAACAC TCCATCGAAG TTCCAGGTGC TGTCAAGTTG 360
TGTAATGCTT TGAACGCCTT GCCAAAGGAA AAATGGGCTG TCGCCACCTC TGGTACCCGT 420
GACATGGCCA AGAAATGGTT CGACATTTTG AAGATCAAGA GACCAGAATA CTTTCATCACC 480
GCCAATGATG TCAAGCAAGG TAAGCCTCAC CCAGAACCAT ACTTAAAGGG TAGAAACGGT 540
TTGGGTTTCC CAATTAATGA ACAAGACCCA TCCAAATCTA AGGTTGTTGT CTTTGAAGAC 600
GCACCAGCTG GTATTGCTGC TGGTAAGGCT GCTGGCTGTA AAATCGTTGG TATTGCTACC 660
ACTTTCGATT TGGACTTCTT GAAGGAAAAG GGTGTGACA TCATTGTCAA GAACCACGAA 720
TCTATCAGAG TCGGTGAATA CAACGCTGAA ACCGATGAAG TCGAATTGAT CTTTGATGAC 780
TACTTATACG CTAAGGATGA CTTGTTGAAA TGGTAA 816

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGGATTGA CTAATAAACC TCTATCTTTG AAAGTTAACG CCGCTTTGTT CGACGTCGAC 60
GGTACCATTA TCATCTCTCA ACCAGCCATT GCTGCATTCT GGAGGGATTT CGGTAAGGAC 120
AAACCTTATT TCGATGCTGA ACACGTTATC CAAGTCTCGC ATGGTTGGAG AACGTTTGAT 180

AACGAACCCA	CGTTGAAGTT	CCCCAAACCG	GGTTGGGTTG	AGTGCCATCC	GCAGAAATTA	840
CTGGTGAACG	TCGTCCAATG	CCTTGCCTCA	AGTTTGCTCT	CTCTGCAGAC	TATCAACAGC	900
GAACGTGTAG	CAAACGGTCT	CCCACCTTAC	AAGGTAATAT	GCATGGGTAT	AGCAAACATG	960
AGAGAAACCA	CAATTCTGTG	GTCCCGCCGC	ACAGGAAAAC	CAATTGTTAA	CTACGGTATT	1020
GTTTGGAACG	ACACCAGAAC	GATCAAAATC	GTTAGAGACA	AATGGCAAAA	CACTAGCGTC	1080
GATAGGCAAC	TGCAGCTTAG	ACAGAAGACT	GGATTGCCAT	TGCTCTCCAC	GTATTTCTCC	1140
TGTTCCAAGC	TGCGCTGGTT	CCTCGACAAT	GAGCCTCTGT	GTACCAAGGC	GTATGAGGAG	1200
AACGACCTGA	TGTTCGGCAC	TGTGGACACA	TGGCTGATTT	ACCAATTAAC	TAAACAAAAG	1260
GCGTTCGTTT	CTGACGTAAC	CAACGCTTCC	AGAACTGGAT	TTATGAACCT	CTCCACTTTA	1320
AAGTACGACA	ACGAGTTGCT	GGAATTTTGG	GGTATTGACA	AGAACCTGAT	TCACATGCCC	1380
GAAATTGTGT	CCTCATCTCA	ATACTACGGT	GACTTTGGCA	TTCCTGATTG	GATAATGGAA	1440
AAGCTACACG	ATTCGCCAAA	AACAGTACTG	CGAGATCTAG	TCAAGAGAAA	CCTGCCCATTA	1500
CAGGGCTGTC	TGGGCGACCA	AAGCGCATCC	ATGGTGGGGC	AACTCGCTTA	CAAACCCGGT	1560
GCTGCAAAAT	GTACTTATGG	TACCGGTTGC	TTTTTACTGT	ACAATACGGG	GACCAAAAAA	1620
TTGATCTCCC	AACATGGCGC	ACTGACGACT	CTAGCATTTT	GGTTCCCACA	TTTGCAAGAG	1680
TACGGTGGCC	AAAAACCAGA	ATTGAGCAAG	CCACATTTTG	CATTAGAGGG	TTCCGTCGCT	1740
GTGGCTGGTG	CTGTGGTCCA	ATGGCTACGT	GATAATTTAC	GATTGATCGA	TAAATCAGAG	1800
GATGTCGGAC	CGATTGCATC	TACGGTTCCT	GATTCTGGTG	GCGTAGTTTT	CGTCCCCGCA	1860
TTTAGTGGCC	TATTGCTCC	CTATTGGGAC	CCAGATGCCA	GAGCCACCAT	AATGGGGATG	1920
TCTCAATTCA	CTACTGCCTC	CCACATCGCC	AGAGCTGCCG	TGGAAGGTGT	TTGCTTTCAA	1980
GCCAGGGCTA	TCTTGAAGGC	AATGAGTTCT	GACGCGTTTG	GTGAAGGTTC	CAAAGACAGG	2040
GACTTTTTAG	AGGAAATTTT	CGACGTCACA	TATGAAAAGT	CGCCCCTGTC	GGTTCTGGCA	2100
GTGGATGGCG	GGATGTCGAG	GTCTAATGAA	GTCATGCAAA	TTCAAGCCGA	TATCCTAGGT	2160
CCCTGTGTCA	AAGTCAGAAG	GTCTCCGACA	GCGGAATGTA	CCGCATTGGG	GGCAGCCATT	2220
GCAGCCAATA	TGGCTTTCAA	GGATGTGAAC	GAGCGCCCAT	TATGGAAGGA	CCTACACGAT	2280
GTTAAGAAAT	GGGTCTTTTA	CAATGGAATG	GAGAAAAACG	AACAAATATC	ACCAGAGGCT	2340
CATCCAAACC	TTAAGATATT	CAGAAGTGAA	TCCGACGATG	CTGAAAGGAG	AAAGCATTGG	2400
AAGTATTGGG	AAGTTGCCGT	GGAAAGATCC	AAAGGTTGGC	TGAAGGACAT	AGAAGGTGAA	2460
CACGAACAGG	TTCTAGAAAA	CTTCCAATAA	CAACATAAAT	AATTTCTATT	AACAATGTAA	2520

[illegible]

Cys	Gly	Ala	Leu	Lys 245	Asn	Val	Val	Ala	Leu 250	Gly	Cys	Gly	Phe	Val 255	Glu
Gly	Leu	Gly	Trp 260	Gly	Asn	Asn	Ala	Ser 265	Ala	Ala	Ile	Gln	Arg 270	Val	Gly
Leu	Gly	Glu 275	Ile	Ile	Arg	Phe	Gly 280	Gln	Met	Phe	Phe	Pro 285	Glu	Ser	Arg
Glu	Glu 290	Thr	Tyr	Tyr	Gln	Glu 295	Ser	Ala	Gly	Val	Ala 300	Asp	Leu	Ile	Thr
Thr 305	Cys	Ala	Gly	Gly	Arg 310	Asn	Val	Lys	Val	Ala 315	Arg	Leu	Met	Ala	Thr 320
Ser	Gly	Lys	Asp	Ala 325	Trp	Glu	Cys	Glu	Lys 330	Glu	Leu	Leu	Asn	Gly 335	Gln
Ser	Ala	Gln	Gly 340	Leu	Ile	Thr	Cys	Lys 345	Glu	Val	His	Glu	Trp 350	Leu	Glu
Thr	Cys	Gly 355	Ser	Val	Glu	Asp	Phe 360	Pro	Leu	Phe	Glu	Ala 365	Val	Tyr	Gln
Ile	Val 370	Tyr	Asn	Asn	Tyr	Pro 375	Met	Lys	Asn	Leu	Pro 380	Asp	Met	Ile	Glu
Glu 385	Leu	Asp	Leu	His	Glu 390	Asp									

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(i)  SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 384 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: unknown
      (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
```

Met 1	Thr	Ala	His 5	Thr	Asn	Ile	Lys	Gln	His 10	Lys	His	Cys	His	Glu 15	Asp
His	Pro	Ile	Arg 20	Arg	Ser	Asp	Ser	Ala 25	Val	Ser	Ile	Val	His 30	Leu	Lys
Arg	Ala	Pro 35	Phe	Lys	Val	Thr	Val 40	Ile	Gly	Ser	Gly	Asn 45	Trp	Gly	Thr
Thr 50	Ile	Ala	Lys	Val	Ile 55	Ala	Glu	Asn	Thr	Glu	Leu 60	His	Ser	His	Ile
Phe 65	Glu	Pro	Glu	Val 70	Arg	Met	Trp	Val	Phe	Asp 75	Glu	Lys	Ile	Gly	Asp 80

Glu Asn Leu Thr Asp Ile Ile Asn Thr Arg His Gln Asn Val Lys Tyr
 85 90 95
 Leu Pro Asn Ile Asp Leu Pro His Asn Leu Val Ala Asp Pro Asp Leu
 100 105 110
 Leu His Ser Ile Lys Gly Ala Asp Ile Leu Val Phe Asn Ile Pro His
 115 120 125
 Gln Phe Leu Pro Asn Ile Val Lys Gln Leu Gln Gly His Val Ala Pro
 130 135 140
 His Val Arg Ala Ile Ser Cys Leu Lys Gly Phe Glu Leu Gly Ser Lys
 145 150 155 160
 Gly Val Gln Leu Leu Ser Ser Tyr Val Thr Asp Glu Leu Gly Ile Gln
 165 170 175
 Cys Gly Ala Leu Ser Gly Ala Asn Leu Ala Pro Glu Val Ala Lys Glu
 180 185 190
 His Trp Ser Glu Thr Thr Val Ala Tyr Gln Leu Pro Lys Asp Tyr Gln
 195 200 205
 Gly Asp Gly Lys Asp Val Asp His Lys Ile Leu Lys Leu Leu Phe His
 210 215 220
 Arg Pro Tyr Phe His Val Asn Val Ile Asp Asp Val Ala Gly Ile Ser
 225 230 235 240
 Ile Ala Gly Ala Leu Lys Asn Val Val Ala Leu Ala Cys Gly Phe Val
 245 250 255
 Glu Gly Met Gly Trp Gly Asn Asn Ala Ser Ala Ala Ile Gln Arg Leu
 260 265 270
 Gly Leu Gly Glu Ile Ile Lys Phe Gly Arg Met Phe Phe Pro Glu Ser
 275 280 285
 Lys Val Glu Thr Tyr Tyr Gln Glu Ser Ala Gly Val Ala Asp Leu Ile
 290 295 300
 Thr Thr Cys Ser Gly Gly Arg Asn Val Lys Val Ala Thr Tyr Met Ala
 305 310 315 320
 Lys Thr Gly Lys Ser Ala Leu Glu Ala Glu Lys Glu Leu Leu Asn Gly
 325 330 335
 Gln Ser Ala Gln Gly Ile Ile Thr Cys Arg Glu Val His Glu Trp Leu
 340 345 350
 Gln Thr Cys Glu Leu Thr Gln Glu Phe Pro Ile Ile Arg Gly Ser Leu
 355 360 365
 Pro Asp Ser Leu Gln Gln Arg Pro His Gly Arg Pro Thr Gly Asp Asp
 370 375 380

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 614 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Met Thr Arg Ala Thr Trp Cys Asn Ser Pro Pro Pro Leu His Arg Gln
1           5           10           15

Val Ser Arg Arg Asp Leu Leu Asp Arg Leu Asp Lys Thr His Gln Phe
20           25           30

Asp Val Leu Ile Ile Gly Gly Gly Ala Thr Gly Thr Gly Cys Ala Leu
35           40           45

Asp Ala Ala Thr Arg Gly Leu Asn Val Ala Leu Val Glu Lys Gly Asp
50           55           60

Phe Ala Ser Gly Thr Ser Ser Lys Ser Thr Lys Met Ile His Gly Gly
65           70           75           80

Val Arg Tyr Leu Glu Lys Ala Phe Trp Glu Phe Ser Lys Ala Gln Leu
85           90           95

Asp Leu Val Ile Glu Ala Leu Asn Glu Arg Lys His Leu Ile Asn Thr
100          105          110

Ala Pro His Leu Cys Thr Val Leu Pro Ile Leu Ile Pro Ile Tyr Ser
115          120          125

Thr Trp Gln Val Pro Tyr Ile Tyr Met Gly Cys Lys Phe Tyr Asp Phe
130          135          140

Phe Gly Gly Ser Gln Asn Leu Lys Lys Ser Tyr Leu Leu Ser Lys Ser
145          150          155          160

Ala Thr Val Glu Lys Ala Pro Met Leu Thr Thr Asp Asn Leu Lys Ala
165          170          175

Ser Leu Val Tyr His Asp Gly Ser Phe Asn Asp Ser Arg Leu Asn Ala
180          185          190

Thr Leu Ala Ile Thr Gly Val Glu Asn Gly Ala Thr Val Leu Ile Tyr
195          200          205

Val Glu Val Gln Lys Leu Ile Lys Asp Pro Thr Ser Gly Lys Val Ile
210          215          220

Gly Ala Glu Ala Arg Asp Val Glu Thr Asn Glu Leu Val Arg Ile Asn
225          230          235          240

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00605735-102500

Ala Lys Cys Val Val Asn Ala Thr Gly Pro Tyr Ser Asp Ala Ile Leu
 245 250 255
 Gln Met Asp Arg Asn Pro Ser Gly Leu Pro Asp Ser Pro Leu Asn Asp
 260 265 270
 Asn Ser Lys Ile Lys Ser Thr Phe Asn Gln Ile Ser Val Met Asp Pro
 275 280 285
 Lys Met Val Ile Pro Ser Ile Gly Val His Ile Val Leu Pro Ser Phe
 290 295 300
 Tyr Ser Pro Lys Asp Met Gly Leu Leu Asp Val Arg Thr Ser Asp Gly
 305 310 315 320
 Arg Val Met Phe Phe Leu Pro Trp Gln Gly Lys Val Leu Ala Gly Thr
 325 330 335
 Thr Asp Ile Pro Leu Lys Gln Val Pro Glu Asn Pro Met Pro Thr Glu
 340 345 350
 Ala Asp Ile Gln Asp Ile Leu Lys Glu Leu Gln His Tyr Ile Glu Phe
 355 360 365
 Pro Val Lys Arg Glu Asp Val Leu Ser Ala Trp Ala Gly Val Arg Pro
 370 375 380
 Leu Val Arg Asp Pro Arg Thr Ile Pro Ala Asp Gly Lys Lys Gly Ser
 385 390 395 400
 Ala Thr Gln Gly Val Val Arg Ser His Phe Leu Phe Thr Ser Asp Asn
 405 410 415
 Gly Leu Ile Thr Ile Ala Gly Gly Lys Trp Thr Thr Tyr Arg Gln Met
 420 425 430
 Ala Glu Glu Thr Val Asp Lys Val Val Glu Val Gly Gly Phe His Asn
 435 440 445
 Leu Lys Pro Cys His Thr Arg Asp Ile Lys Leu Ala Gly Ala Glu Glu
 450 455 460
 Trp Thr Gln Asn Tyr Val Ala Leu Leu Ala Gln Asn Tyr His Leu Ser
 465 470 475 480
 Ser Lys Met Ser Asn Tyr Leu Val Gln Asn Tyr Gly Thr Arg Ser Ser
 485 490 495
 Ile Ile Cys Glu Phe Phe Lys Glu Ser Met Glu Asn Lys Leu Pro Leu
 500 505 510
 Ser Leu Ala Asp Lys Glu Asn Asn Val Ile Tyr Ser Ser Glu Glu Asn
 515 520 525
 Asn Leu Val Asn Phe Asp Thr Phe Arg Tyr Pro Phe Thr Ile Gly Glu
 530 535 540

Leu Lys Tyr Ser Met Gln Tyr Glu Tyr Cys Arg Thr Pro Leu Asp Phe
 545 550 555 560
 Leu Leu Arg Arg Thr Arg Phe Ala Phe Leu Asp Ala Lys Glu Ala Leu
 565 570 575
 Asn Ala Val His Ala Thr Val Lys Val Met Gly Asp Glu Phe Asn Trp
 580 585 590
 Ser Glu Lys Lys Arg Gln Trp Glu Leu Glu Lys Thr Val Asn Phe Ile
 595 600 605
 Gln Gly Arg Phe Gly Val
 610

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Asn Gln Arg Asn Ala Ser Met Thr Val Ile Gly Ala Gly Ser Tyr
 1 5 10 15
 Gly Thr Ala Leu Ala Ile Thr Leu Ala Arg Asn Gly His Glu Val Val
 20 25 30
 Leu Trp Gly His Asp Pro Glu His Ile Ala Thr Leu Glu Arg Asp Arg
 35 40 45
 Cys Asn Ala Ala Phe Leu Pro Asp Val Pro Phe Pro Asp Thr Leu His
 50 55 60
 Leu Glu Ser Asp Leu Ala Thr Ala Leu Ala Ala Ser Arg Asn Ile Leu
 65 70 75 80
 Val Val Val Pro Ser His Val Phe Gly Glu Val Leu Arg Gln Ile Lys
 85 90 95
 Pro Leu Met Arg Pro Asp Ala Arg Leu Val Trp Ala Thr Lys Gly Leu
 100 105 110
 Glu Ala Glu Thr Gly Arg Leu Leu Gln Asp Val Ala Arg Glu Ala Leu
 115 120 125
 Gly Asp Gln Ile Pro Leu Ala Val Ile Ser Gly Pro Thr Phe Ala Lys
 130 135 140
 Glu Leu Ala Ala Gly Leu Pro Thr Ala Ile Ser Leu Ala Ser Thr Asp
 145 150 155 160

Gln Thr Phe Ala Asp Asp Leu Gln Gln Leu Leu His Cys Gly Lys Ser
 165 170 175
 Phe Arg Val Tyr Ser Asn Pro Asp Phe Ile Gly Val Gln Leu Gly Gly
 180 185 190
 Ala Val Lys Asn Val Ile Ala Ile Gly Ala Gly Met Ser Asp Gly Ile
 195 200 205
 Gly Phe Gly Ala Asn Ala Arg Thr Ala Leu Ile Thr Arg Gly Leu Ala
 210 215 220
 Glu Met Ser Arg Leu Gly Ala Ala Leu Gly Ala Asp Pro Ala Thr Phe
 225 230 235 240
 Met Gly Met Ala Gly Leu Gly Asp Leu Val Leu Thr Cys Thr Asp Asn
 245 250 255
 Gln Ser Arg Asn Arg Arg Phe Gly Met Met Leu Gly Gln Gly Met Asp
 260 265 270
 Val Gln Ser Ala Gln Glu Lys Ile Gly Gln Val Val Glu Gly Tyr Arg
 275 280 285
 Asn Thr Lys Glu Val Arg Glu Leu Ala His Arg Phe Gly Val Glu Met
 290 295 300
 Pro Ile Thr Glu Glu Ile Tyr Gln Val Leu Tyr Cys Gly Lys Asn Ala
 305 310 315 320
 Arg Glu Ala Ala Leu Thr Leu Leu Gly Arg Ala Arg Lys Asp Glu Arg
 325 330 335
 Ser Ser His

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 501 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Glu Thr Lys Asp Leu Ile Val Ile Gly Gly Gly Ile Asn Gly Ala
 1 5 10 15
 Gly Ile Ala Ala Asp Ala Ala Gly Arg Gly Leu Ser Val Leu Met Leu
 20 25 30
 Glu Ala Gln Asp Leu Ala Cys Ala Thr Ser Ser Ala Ser Ser Lys Leu
 35 40 45
 Ile His Gly Gly Leu Arg Tyr Leu Glu His Tyr Glu Phe Arg Leu Val
 50 55 60

Ser Glu Ala Leu Ala Glu Arg Glu Val Leu Leu Lys Met Ala Pro His
 65 70 75 80
 Ile Ala Phe Pro Met Arg Phe Arg Leu Pro His Arg Pro His Leu Arg
 85 90 95
 Pro Ala Trp Met Ile Arg Ile Gly Leu Phe Met Tyr Asp His Leu Gly
 100 105 110
 Lys Arg Thr Ser Leu Pro Gly Ser Thr Gly Leu Arg Phe Gly Ala Asn
 115 120 125
 Ser Val Leu Lys Pro Glu Ile Lys Arg Gly Phe Glu Tyr Ser Asp Cys
 130 135 140
 Trp Val Asp Asp Ala Arg Leu Val Leu Ala Asn Ala Gln Met Val Val
 145 150 155 160
 Arg Lys Gly Gly Glu Val Leu Thr Arg Thr Arg Ala Thr Ser Ala Arg
 165 170 175
 Arg Glu Asn Gly Leu Trp Ile Val Glu Ala Glu Asp Ile Asp Thr Gly
 180 185 190
 Lys Lys Tyr Ser Trp Gln Ala Arg Gly Leu Val Asn Ala Thr Gly Pro
 195 200 205
 Trp Val Lys Gln Phe Phe Asp Asp Gly Met His Leu Pro Ser Pro Tyr
 210 215 220
 Gly Ile Arg Leu Ile Lys Gly Ser His Ile Val Val Pro Arg Val His
 225 230 235 240
 Thr Gln Lys Gln Ala Tyr Ile Leu Gln Asn Glu Asp Lys Arg Ile Val
 245 250 255
 Phe Val Ile Pro Trp Met Asp Glu Phe Ser Ile Ile Gly Thr Thr Asp
 260 265 270
 Val Glu Tyr Lys Gly Asp Pro Lys Ala Val Lys Ile Glu Glu Ser Glu
 275 280 285
 Ile Asn Tyr Leu Leu Asn Val Tyr Asn Thr His Phe Lys Lys Gln Leu
 290 295 300
 Ser Arg Asp Asp Ile Val Trp Thr Tyr Ser Gly Val Arg Pro Leu Cys
 305 310 315 320
 Asp Asp Glu Ser Asp Ser Pro Gln Ala Ile Thr Arg Asp Tyr Thr Leu
 325 330 335
 Asp Ile His Asp Glu Asn Gly Lys Ala Pro Leu Leu Ser Val Phe Gly
 340 345 350
 Gly Lys Leu Thr Thr Tyr Arg Lys Leu Ala Glu His Ala Leu Glu Lys
 355 360 365

Leu Thr Pro Tyr Tyr Gln Gly Ile Gly Pro Ala Trp Thr Lys Glu Ser
 370 375 380
 Val Leu Pro Gly Gly Ala Ile Glu Gly Asp Arg Asp Asp Tyr Ala Ala
 385 390 395 400
 Arg Leu Arg Arg Arg Tyr Pro Phe Leu Thr Glu Ser Leu Ala Arg His
 405 410 415
 Tyr Ala Arg Thr Tyr Gly Ser Asn Ser Glu Leu Leu Leu Gly Asn Ala
 420 425 430
 Gly Thr Val Ser Asp Leu Gly Glu Asp Phe Gly His Glu Phe Tyr Glu
 435 440 445
 Ala Glu Leu Lys Tyr Leu Val Asp His Glu Trp Val Arg Arg Ala Asp
 450 455 460
 Asp Ala Leu Trp Arg Arg Thr Lys Gln Gly Met Trp Leu Asn Ala Asp
 465 470 475 480
 Gln Gln Ser Arg Val Ser Gln Trp Leu Val Glu Tyr Thr Gln Gln Arg
 485 490 495
 Leu Ser Leu Ala Ser
 500

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Lys Thr Arg Asp Ser Gln Ser Ser Asp Val Ile Ile Ile Gly Gly
 1 5 10 15
 Gly Ala Thr Gly Ala Gly Ile Ala Arg Asp Cys Ala Leu Arg Gly Leu
 20 25 30
 Arg Val Ile Leu Val Glu Arg His Asp Ile Ala Thr Gly Ala Thr Gly
 35 40 45
 Arg Asn His Gly Leu Leu His Ser Gly Ala Arg Tyr Ala Val Thr Asp
 50 55 60
 Ala Glu Ser Ala Arg Glu Cys Ile Ser Glu Asn Gln Ile Leu Lys Arg
 65 70 75 80
 Ile Ala Arg His Cys Val Glu Pro Thr Asn Gly Leu Phe Ile Thr Leu
 85 90 95

Pro Glu Asp Asp Leu Ser Phe Gln Ala Thr Phe Ile Arg Ala Cys Glu
 100 105 110
 Glu Ala Gly Ile Ser Ala Glu Ala Ile Asp Pro Gln Gln Ala Arg Ile
 115 120 125
 Ile Glu Pro Ala Val Asn Pro Ala Leu Ile Gly Ala Val Lys Val Pro
 130 135 140
 Asp Gly Thr Val Asp Pro Phe Arg Leu Thr Ala Ala Asn Met Leu Asp
 145 150 155 160
 Ala Lys Glu His Gly Ala Val Ile Leu Thr Ala His Glu Val Thr Gly
 165 170 175
 Leu Ile Arg Glu Gly Ala Thr Val Cys Gly Val Arg Val Arg Asn His
 180 185 190
 Leu Thr Gly Glu Thr Gln Ala Leu His Ala Pro Val Val Val Asn Ala
 195 200 205
 Ala Gly Ile Trp Gly Gln His Ile Ala Glu Tyr Ala Asp Leu Arg Ile
 210 215 220
 Arg Met Phe Pro Ala Lys Gly Ser Leu Leu Ile Met Asp His Arg Ile
 225 230 235 240
 Asn Gln His Val Ile Asn Arg Cys Arg Lys Pro Ser Asp Ala Asp Ile
 245 250 255
 Leu Val Pro Gly Asp Thr Ile Ser Leu Ile Gly Thr Thr Ser Leu Arg
 260 265 270
 Ile Asp Tyr Asn Glu Ile Asp Asp Asn Arg Val Thr Ala Glu Glu Val
 275 280 285
 Asp Ile Leu Leu Arg Glu Gly Glu Lys Leu Ala Pro Val Met Ala Lys
 290 295 300
 Thr Arg Ile Leu Arg Ala Tyr Ser Gly Val Arg Pro Leu Val Ala Ser
 305 310 315 320
 Asp Asp Asp Pro Ser Gly Arg Asn Leu Ser Arg Gly Ile Val Leu Leu
 325 330 335
 Asp His Ala Glu Arg Asp Gly Leu Asp Gly Phe Ile Thr Ile Thr Gly
 340 345 350
 Gly Lys Leu Met Thr Tyr Arg Leu Met Ala Glu Trp Ala Thr Asp Ala
 355 360 365
 Val Cys Arg Lys Leu Gly Asn Thr Arg Pro Cys Thr Thr Ala Asp Leu
 370 375 380
 Ala Leu Pro Gly Ser Gln Glu Pro Ala Glu Val Thr Leu Arg Lys Val
 385 390 395 400

Ile Ser Leu Pro Ala Pro Leu Arg Gly Ser Ala Val Tyr Arg His Gly
 405 410 415
 Asp Arg Thr Pro Ala Trp Leu Ser Glu Gly Arg Leu His Arg Ser Leu
 420 425 430
 Val Cys Glu Cys Glu Ala Val Thr Ala Gly Glu Val Gln Tyr Ala Val
 435 440 445
 Glu Asn Leu Asn Val Asn Ser Leu Leu Asp Leu Arg Arg Arg Thr Arg
 450 455 460
 Val Gly Met Gly Thr Cys Gln Gly Glu Leu Cys Ala Cys Arg Ala Ala
 465 470 475 480
 Gly Leu Leu Gln Arg Phe Asn Val Thr Thr Ser Ala Gln Ser Ile Glu
 485 490 495
 Gln Leu Ser Thr Phe Leu Asn Glu Arg Trp Lys Gly Val Gln Pro Ile
 500 505 510
 Ala Trp Gly Asp Ala Leu Arg Glu Ser Glu Phe Thr Arg Trp Val Tyr
 515 520 525
 Gln Gly Leu Cys Gly Leu Glu Lys Glu Gln Lys Asp Ala Leu
 530 535 540

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 250 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Gly Leu Thr Thr Lys Pro Leu Ser Leu Lys Val Asn Ala Ala Leu
 1 5 10 15
 Phe Asp Val Asp Gly Thr Ile Ile Ile Ser Gln Pro Ala Ile Ala Ala
 20 25 30
 Phe Trp Arg Asp Phe Gly Lys Asp Lys Pro Tyr Phe Asp Ala Glu His
 35 40 45
 Val Ile Gln Val Ser His Gly Trp Arg Thr Phe Asp Ala Ile Ala Lys
 50 55 60
 Phe Ala Pro Asp Phe Ala Asn Glu Glu Tyr Val Asn Lys Leu Glu Ala
 65 70 75 80
 Glu Ile Pro Val Lys Tyr Gly Glu Lys Ser Ile Glu Val Pro Gly Ala
 85 90 95

Val Lys Leu Cys Asn Ala Leu Asn Ala Leu Pro Lys Glu Lys Trp Ala
100 105 110

Val Ala Thr Ser Gly Thr Arg Asp Met Ala Gln Lys Trp Phe Glu His
115 120 125

Leu Gly Ile Arg Arg Pro Lys Tyr Phe Ile Thr Ala Asn Asp Val Lys
130 135 140

Gln Gly Lys Pro His Pro Glu Pro Tyr Leu Lys Gly Arg Asn Gly Leu
145 150 155 160

Gly Tyr Pro Ile Asn Glu Gln Asp Pro Ser Lys Ser Lys Val Val Val
165 170 175

Phe Glu Asp Ala Pro Ala Gly Ile Ala Ala Gly Lys Ala Ala Gly Cys
180 185 190

Lys Ile Ile Gly Ile Ala Thr Thr Phe Asp Leu Asp Phe Leu Lys Glu
195 200 205

Lys Gly Cys Asp Ile Ile Val Lys Asn His Glu Ser Ile Arg Val Gly
210 215 220

Gly Tyr Asn Ala Glu Thr Asp Glu Val Glu Phe Ile Phe Asp Asp Tyr
225 230 235 240

Leu Tyr Ala Lys Asp Asp Leu Leu Lys Trp
245 250

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Lys Arg Phe Asn Val Leu Lys Tyr Ile Arg Thr Thr Lys Ala Asn
1 5 10 15

Ile Gln Thr Ile Ala Met Pro Leu Thr Thr Lys Pro Leu Ser Leu Lys
20 25 30

Ile Asn Ala Ala Leu Phe Asp Val Asp Gly Thr Ile Ile Ile Ser Gln
35 40 45

Pro Ala Ile Ala Ala Phe Trp Arg Asp Phe Gly Lys Asp Lys Pro Tyr
50 55 60

Phe Asp Ala Glu His Val Ile His Ile Ser His Gly Trp Arg Thr Tyr
65 70 75 80

Asp Ala Ile Ala Lys Phe Ala Pro Asp Phe Ala Asp Glu Glu Tyr Val
 85 90 95
 Asn Lys Leu Glu Gly Glu Ile Pro Glu Lys Tyr Gly Glu His Ser Ile
 100 105 110
 Glu Val Pro Gly Ala Val Lys Leu Cys Asn Ala Leu Asn Ala Leu Pro
 115 120 125
 Lys Glu Lys Trp Ala Val Ala Thr Ser Gly Thr Arg Asp Met Ala Lys
 130 135 140
 Lys Trp Phe Asp Ile Leu Lys Ile Lys Arg Pro Glu Tyr Phe Ile Thr
 145 150 155 160
 Ala Asn Asp Val Lys Gln Gly Lys Pro His Pro Glu Pro Tyr Leu Lys
 165 170 175
 Gly Arg Asn Gly Leu Gly Phe Pro Ile Asn Glu Gln Asp Pro Ser Lys
 180 185 190
 Ser Lys Val Val Val Phe Glu Asp Ala Pro Ala Gly Ile Ala Ala Gly
 195 200 205
 Lys Ala Ala Gly Cys Lys Ile Val Gly Ile Ala Thr Thr Phe Asp Leu
 210 215 220
 Asp Phe Leu Lys Glu Lys Gly Cys Asp Ile Ile Val Lys Asn His Glu
 225 230 235 240
 Ser Ile Arg Val Gly Glu Tyr Asn Ala Glu Thr Asp Glu Val Glu Leu
 245 250 255
 Ile Phe Asp Asp Tyr Leu Tyr Ala Lys Asp Asp Leu Leu Lys Trp
 260 265 270

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 709 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Phe Pro Ser Leu Phe Arg Leu Val Val Phe Ser Lys Arg Tyr Ile
 1 5 10 15
 Phe Arg Ser Ser Gln Arg Leu Tyr Thr Ser Leu Lys Gln Glu Gln Ser
 20 25 30
 Arg Met Ser Lys Ile Met Glu Asp Leu Arg Ser Asp Tyr Val Pro Leu
 35 40 45

Ile Ala Ser Ile Asp Val Gly Thr Thr Ser Ser Arg Cys Ile Leu Phe
 50 55 60
 Asn Arg Trp Gly Gln Asp Val Ser Lys His Gln Ile Glu Tyr Ser Thr
 65 70 75 80
 Ser Ala Ser Lys Gly Lys Ile Gly Val Ser Gly Leu Arg Arg Pro Ser
 85 90 95
 Thr Ala Pro Ala Arg Glu Thr Pro Asn Ala Gly Asp Ile Lys Thr Ser
 100 105 110
 Gly Lys Pro Ile Phe Ser Ala Glu Gly Tyr Ala Ile Gln Glu Thr Lys
 115 120 125
 Phe Leu Lys Ile Glu Glu Leu Asp Leu Asp Phe His Asn Glu Pro Thr
 130 135 140
 Leu Lys Phe Pro Lys Pro Gly Trp Val Glu Cys His Pro Gln Lys Leu
 145 150 155 160
 Leu Val Asn Val Val Gln Cys Leu Ala Ser Ser Leu Leu Ser Leu Gln
 165 170 175
 Thr Ile Asn Ser Glu Arg Val Ala Asn Gly Leu Pro Pro Tyr Lys Val
 180 185 190
 Ile Cys Met Gly Ile Ala Asn Met Arg Glu Thr Thr Ile Leu Trp Ser
 195 200 205
 Arg Arg Thr Gly Lys Pro Ile Val Asn Tyr Gly Ile Val Trp Asn Asp
 210 215 220
 Thr Arg Thr Ile Lys Ile Val Arg Asp Lys Trp Gln Asn Thr Ser Val
 225 230 235 240
 Asp Arg Gln Leu Gln Leu Arg Gln Lys Thr Gly Leu Pro Leu Leu Ser
 245 250 255
 Thr Tyr Phe Ser Cys Ser Lys Leu Arg Trp Phe Leu Asp Asn Glu Pro
 260 265 270
 Leu Cys Thr Lys Ala Tyr Glu Glu Asn Asp Leu Met Phe Gly Thr Val
 275 280 285
 Asp Thr Trp Leu Ile Tyr Gln Leu Thr Lys Gln Lys Ala Phe Val Ser
 290 295 300
 Asp Val Thr Asn Ala Ser Arg Thr Gly Phe Met Asn Leu Ser Thr Leu
 305 310 315 320
 Lys Tyr Asp Asn Glu Leu Leu Glu Phe Trp Gly Ile Asp Lys Asn Leu
 325 330 335
 Ile His Met Pro Glu Ile Val Ser Ser Ser Gln Tyr Tyr Gly Asp Phe
 340 345 350

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355 360 365
Val Leu Asp Leu Val Lys Arg Asn Leu Phe Ile Gln Gly Cys Leu
370 375 380
Gly Asp Gln Ser Ala Ser Met Val Gly Gln Leu Ala Tyr Lys Pro Gly
385 390 395 400
Ala Ala Lys Cys Thr Tyr Gly Thr Gly Cys Phe Leu Leu Tyr Asn Thr
405 410 415
Gly Thr Lys Lys Leu Ile Ser Gln His Gly Ala Leu Thr Thr Leu Ala
420 425 430
Phe Trp Phe Pro His Leu Gln Glu Tyr Gly Gly Gln Lys Pro Glu Leu
435 440 445
Ser Lys Pro His Phe Ala Leu Glu Gly Ser Val Ala Val Ala Gly Ala
450 455 460
Val Val Gln Trp Leu Arg Asp Asn Leu Arg Leu Ile Asp Lys Ser Glu
465 470 475 480
Asp Val Gly Pro Ile Ala Ser Thr Val Pro Asp Ser Gly Gly Val Val
485 490 495
Phe Val Pro Ala Phe Ser Gly Leu Phe Ala Pro Tyr Trp Asp Pro Asp
500 505 510
Ala Arg Ala Thr Ile Met Gly Met Ser Gln Phe Thr Thr Ala Ser His
515 520 525
Ile Ala Arg Ala Ala Val Glu Gly Val Cys Phe Gln Ala Arg Ala Ile
530 535 540
Leu Lys Ala Met Ser Ser Asp Ala Phe Gly Glu Gly Ser Lys Asp Arg
545 550 555 560
Asp Phe Leu Glu Glu Ile Ser Asp Val Thr Tyr Glu Lys Ser Pro Leu
565 570 575
Ser Val Leu Ala Val Asp Gly Gly Met Ser Arg Ser Asn Glu Val Met
580 585 590
Gln Ile Gln Ala Asp Ile Leu Gly Pro Cys Val Lys Val Arg Arg Ser
595 600 605
Pro Thr Ala Glu Cys Thr Ala Leu Gly Ala Ala Ile Ala Ala Asn Met
610 615 620
Ala Phe Lys Asp Val Asn Glu Arg Pro Leu Trp Lys Asp Leu His Asp
625 630 635 640
Val Lys Lys Trp Val Phe Tyr Asn Gly Met Glu Lys Asn Glu Gln Ile
645 650 655

Ser Pro Glu Ala His Pro Asn Leu Lys Ile Phe Arg Ser Glu Ser Asp
660 665 670

Asp Ala Glu Arg Arg Lys His Trp Lys Tyr Trp Glu Val Ala Val Glu
675 680 685

Arg Ser Lys Gly Trp Leu Lys Asp Ile Glu Gly Glu His Glu Gln Val
690 695 700

Leu Glu Asn Phe Gln
705

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCGCGGATCC AGGAGTCTAG AATTATGGGA TTGACTACTA AACCTCTATC T 51

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GATACGCCCCG GGTTACCATT TCAACAGATC GTCCTT 36

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTGATAATAT AACCATGGCT GCTGCTGCTG ATAG 34

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTATGATATG TTATCTTGA TCCAATAAAT CTAATCTTC

39

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATGACTAGT AAGGAGGACA ATTC

24

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CATGGAATTG TCCTCCTTAC TAGT

24

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTAGTAAGGA GGACAATTC

19

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CATGGAATTG TCCTCCTTA

19

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GATCCAGGAA ACAGA

15

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTAGTCTGTT TCCTG

15

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCTTTCTGTG CTGCGGCTTT AG

22

- (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGGTCGAGGA TCCAATTAC TTT

23

- (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAAGTGAAGT GGATCCTCGA CCAATTGGAT GGTGGCGCAG TAGCAAACAA T

51

- (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGATCACCGC CGCAGAACT ACG

23

- (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
CTGTCAGCCG TTAAGTGTTT CTGTG 25

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
CAGTTCAACC TGTGATAGT ACG 23

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
ATGAGTCAAA CATCAACCTT 20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
ATGGAGAAAA AAATCACTGG 20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
TTACGCCCCG CCCTGCCACT 20

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TCAGAGGATG TGCACCTGCA

20

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGAGCATGCC GCATTTGGCA CTACTC

26

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CGGTCTAGAG TAGGTTATTC CCACTCTTG

29

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAAGTCGACC GCTGCGCCTT ATCCGG

26

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CGCGTCGACG TTTACAATTT CAGGTGGC

28

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCAGCATGCT GGACTGGTAG TAG

23

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CAGTCTAGAG TTATTGGCAA ACCTACC

27

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATGCATGCC CAGGGCGGAG ACGGC

25

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTAACGATTG TTCTCTAGAG AAAATGTCC

29

00505785 102500